

- 1 -

1 -

The diagram illustrates a protein sequence alignment between two homologous genes. The top sequence is a reference, while the bottom sequence shows specific mutations. Key features include:

- Amino Acid Substitutions:** Red dots indicate changes from the reference sequence.
- Frameshift:** A red dot at position 100 indicates a frameshift mutation.
- Stop Codons:** Red circles at positions 100 and 101 indicate premature stop codons.
- Insertions/Deletions:** Dashes (-) indicate insertions or deletions relative to the reference sequence.

 Windows p35 6.4 bits

•35 6.4 bits

... -----] p35-(21)-p10 2141121 Gap 3.3 bits
-----] p35-p10 2141121 total 6.0 bits

... } p35-(26)-p10 2141126 Gap 3.7 bits

{-----} sd-(7)-ir 2141155 Gap 3.7 bits
{-----} sd-ir 2141155 vdk vegE total 11.8 bits

10 p10 3.8 bits

p10 3.8 bit

----| p35-p10 2141126 total

p35 4.2 bits

{ p35-(22)-p10 2141152 Gap 2.3 bits
|-----| p35-p10 2141152 total 5.7 bits

5' ttt acgtt cactttatgagccaaatctcgatataaaaaatgttaaaaacttttgtaactagcataaaacacaagaaaaacgaaatactggccgac 3'

- phe - thr - ser - leu - tyr - glu - gln - phe - ala - tyr - lys - met -

- - - - fMet - ser - asn - ser - his - ile - lys - cys - lys - thr - phe - val - leu - ala -

- - - - tyr - val - thr - leu -

I II III

[###> orf 16 codons

p35 1.4 bits

p10 4.5 bit

p10 3.5 bits

```
| p35-p10 2141237 total 4.5 bit  
|  
| {  
| p35 3.5 bits
```

